

SEQUENCE LISTING

<110> C. Frank Bennett
Jacqueline Wyatt

<120> ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION

<130> RTS-0147

<160> 176

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<211> 2077

<212> DNA

<213> Homo sapiens

<220>

<220>

<221> CDS

<222> (257) ... (1213)

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 acttctgaga aggttgccga cagctgtgcc cggcagtcta gaggcgaga agaggaagcc 180
 atcgctggc cccggctctc tggaccttgt ctgctcggg agcggaacaa gcggcagcca 240
 gagaactggt ttaatc atg gac aaa caa aac tca cag atg gct tct cac 292
 Met Asp Lys Gln Asn Ser Gln Met Asn Ala Ser His
 1 5 10
 ccg gaa aca aac ttg cca gtt ggg tat cct cct cag tat cca ccg aca 340
 Pro Glu Thr Asn Leu Pro Val Gly Tyr Pro Pro Gln Tyr Pro Pro Thr
 15 20 25
 gca ttc caa gga cct cca gga tat agt ggc tac cct ggg ccc cag gtc 388
 Ala Phe Gln Gly Pro Pro Gly Tyr Ser Gly Tyr Pro Gly Pro Gln Val
 30 35 40
 agc tac cca ccc cca cca gcc ggc cat tca ggt cct ggc cca gct ggc 436
 Ser Tyr Pro Pro Pro Ala Gly His Ser Gly Pro Gly Pro Ala Gly
 45 50 55 60
 ttt cct gtc cca aat cag cca gtg tat aat cag cca gta tat aat cag 484
 Phe Pro Val Pro Asn Gln Pro Val Tyr Asn Gln Pro Val Tyr Asn Gln
 65 70 75
 cca gtt gga gct gca ggg gta cca tgg atg cca gcg cca cag cct cca 532
 Pro Val Gly Ala Ala Gly Val Pro Trp Met Pro Ala Pro Gln Pro Pro
 80 85 90
 tta aac tgt cca cct gga tta gaa tat tta agt cag ata gat cag ata 580
 Leu Asn Cys Pro Pro Gly Leu Glu Tyr Leu Ser Gln Ile Asp Gln Ile

95	100	105	
ctg att cat cag caa att gaa ctt ctg gaa gtt tta aca ggt ttt gaa			628
Leu Ile His Gln Gln Ile Glu Leu Leu Glu Val Leu Thr Gly Phe Glu			
110	115	120	
act aat aac aaa tat gaa att aag aac agc ttt gga cag agg gtt tac			676
Thr Asn Asn Lys Tyr Glu Ile Lys Asn Ser Phe Gly Gln Arg Val Tyr			
125	130	135	140
ttt gca gcg gaa gat act gat tgc tgt acc cga aat tgc tgt ggg cca			724
Phe Ala Ala Glu Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Gly Pro			
145	150	155	
tct aga cct ttt acc ttg agg att att gat aat atg ggt caa gaa gtc			772
Ser Arg Pro Phe Thr Leu Arg Ile Ile Asp Asn Met Gly Gln Glu Val			
160	165	170	
ata act ctg gag aga cca cta aga tgt agc agc tgt tgt tgc ccc tgc			820
Ile Thr Leu Glu Arg Pro Leu Arg Cys Ser Ser Cys Cys Pro Cys			
175	180	185	
tgc ctt cag gag ata gaa atc caa gct cct cct ggt gta cca ata ggt			868
Cys Leu Gln Glu Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly			
190	195	200	
tat gtt att cag act tgg cac cca tgt cta cca aag ttt aca att caa			916
Tyr Val Ile Gln Thr Trp His Pro Cys Leu Pro Lys Phe Thr Ile Gln			
205	210	215	220
aat gag aaa aga gag gat gta cta aaa ata agt ggt cca tgt gtt gtg			964
Asn Glu Lys Arg Glu Asp Val Leu Lys Ile Ser Gly Pro Cys Val Val			
225	230	235	
tgc agc tgt tgt gga gat gtt gat ttt gag att aaa tct ctt gat gaa			1012
Cys Ser Cys Cys Gly Asp Val Asp Phe Glu Ile Lys Ser Leu Asp Glu			
240	245	250	
cag tgt gtg gtt ggc aaa att tcc aag cac tgg act gga att ttg aga			1060
Gln Cys Val Val Gly Lys Ile Ser Lys His Trp Thr Gly Ile Leu Arg			
255	260	265	
gag gca ttt aca gac gct gat aac ttt gga atc cag ttc cct tta gac			1108
Glu Ala Phe Thr Asp Ala Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp			

270 275 280
 ctt gat gtt aaa atg aaa gct gta atg att ggt gcc tgt ttc ctc att 1156
 Leu Asp Val Lys Met Lys Ala Val Met Ile Gly Ala Cys Phe Leu Ile
 285 290 295 300
 gac ttc atg ttt ttt gaa agc act ggc agc cag gaa caa aaa tca gga 1204
 Asp Phe Met Phe Phe Glu Ser Thr Gly Ser Gln Glu Gln Lys Ser Gly
 305 310 315
 gtg tgg tag tggattagtg aaagtctctc caggaaatct gaagtctgta tattgattga 1263
 Val Trp
 gactatctaa actcatacct gtatgaatta agctgtaagg cctgtagctc tggttgtata 1323
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 gtttagctct tacactctat ccttcttaga aaatggtaat tgagattact cagatattaa 1983
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<223> PCR Primer

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ctgtgcgcaa ccttctcaga

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<210> 6
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ttactcccag acccttttcc ggctga

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<210> 7
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<400> 7

gaaggtgaag gtcggagtc

19

<210> 8

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<210> 9

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<400> 9

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<213> Mus musculus

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 agtcgctgct ggtgctagga ttctaggaat tcgcctcact tggagctgca tgagaaaaga 180
 aaggcttgca a atg gag gct cct cgc tca gga aca tac ttg cca gct ggg 230
 Met Glu Ala Pro Arg Ser Gly Thr Tyr Leu Pro Ala Gly
 1 5 10
 tat gcc cct cag tat cct cca gca gca gtc caa gga cct cca gag cat 278
 Tyr Ala Pro Gln Tyr Pro Pro Ala Ala Val Gln Gly Pro Pro Glu His
 15 20 25
 act gga cgc ccc aca ttc cag act aac tac caa gtt ccc cag tct ggt 326
 Thr Gly Arg Pro Thr Phe Gln Thr Asn Tyr Gln Val Pro Gln Ser Gly
 30 35 40 45
 tat cca gga cct cag gct agc tac aca gtc tca aca tct gga cat gaa 374
 Tyr Pro Gly Pro Gln Ala Ser Tyr Thr Val Ser Thr Ser Gly His Glu
 50 55 60
 ggt tat gct gct aca cgg ctt cct att caa aat aat cag act ata gtc 422
 Gly Tyr Ala Ala Thr Arg Leu Pro Ile Gln Asn Asn Gln Thr Ile Val
 65 70 75
 ctt gca aac act cag tgg atg cca gca cca cca cct att ctg aac tgc 470
 Leu Ala Asn Thr Gln Trp Met Pro Ala Pro Pro Pro Ile Leu Asn Cys
 80 85 90
 cca cct ggg cta gaa tac tta aat cag ata gat cag ctt ctg att cat 518
 Pro Pro Gly Leu Glu Tyr Leu Asn Gln Ile Asp Gln Leu Leu Ile His
 95 100 105
 cag caa gtt gaa ctt cta gaa gtc tta aca ggc ttt gaa aca aat aac 566
 Gln Gln Val Glu Leu Leu Glu Val Leu Thr Gly Phe Glu Thr Asn Asn
 110 115 120 125
 aaa ttt gaa atc aag aac agc ctc ggg cag atg gtt tat gtt gca gtg 614
 Lys Phe Glu Ile Lys Asn Ser Leu Gly Gln Met Val Tyr Val Ala Val
 130 135 140
 gaa gat act gac tgc tgt act cga aat tgc tgt gaa gcg tct aga cct 662

Glu Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Glu Ala Ser Arg Pro	
145	150 155
ttc acc tta aga atc ctg gat cat ctg ggc caa gaa gtc atg act ctg	710
Phe Thr Leu Arg Ile Leu Asp His Leu Gly Gln Glu Val Met Thr Leu	
160	165 170
gag cga cct ctg aga tgc agt agc tgc tgc ttc ccc tgc tgc ctc cag	758
Glu Arg Pro Leu Arg Cys Ser Ser Cys Cys Phe Pro Cys Cys Leu Gln	
175	180 185
gag ata gaa atc cag gct cct ccg ggg gtg cca ata ggt tat gtg act	806
Glu Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly Tyr Val Thr	
190	195 200 205
cag acc tgg cac cca tgt ctg cca aag ctc act ctt cag aac gac aag	854
Gln Thr Trp His Pro Cys Leu Pro Lys Leu Thr Leu Gln Asn Asp Lys	
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agg gag aat gtt cta aaa gta gtt ggt cca tgt gtt gca tgc acc tgc	902
Arg Glu Asn Val Leu Lys Val Val Gly Pro Cys Val Ala Cys Thr Cys	
	225 230 235
tgt tca gat att gac ttt gag atc aag tct ctt gat gaa gtg act aga	950
Cys Ser Asp Ile Asp Phe Glu Ile Lys Ser Leu Asp Glu Val Thr Arg	
	240 245 250
att ggt aag atc acc aag cag tgg tct ggt tgt gtg aaa gag gcc ttc	998
Ile Gly Lys Ile Thr Lys Gln Trp Ser Gly Cys Val Lys Glu Ala Phe	
	255 260 265
acg gat tgc gat aac ttt ggg atc caa ttc ccg cta gac ctg gag gtg	1046
Thr Asp Ser Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp Leu Glu Val	
	270 275 280 285
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Lys Met Lys Ala Val Thr Leu Gly Ala Cys Phe Leu Ile Asp Tyr Met	
	290 295 300
ttt ttt gaa ggc tgt gag tag gaacagaaat ccgacctgca gtaggaatca	1145
Phe Phe Glu Gly Cys Glu	
	305
atgaaaggagg acagagaaga tctgaagtct acacaaggagg atcatatgat tgagagacct	1205

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<400> 12

gtgaggcgaa ttectagaat cct

23

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> PCR Probe

<400> 13

agcagcgact cagctctcca gactcct

27

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 14

ggcaaattca acggcacagt

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<210> 15

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ttaaactgtc cacctggatt agaataattta agtcaggtaa tttcaaagac acaaaatact 180
cataaaaaac agaactgtgc ttccagcttg cttaaccaga ttagcaaatg aataattcac 240
caaagtctga aatagcaaaa ctgtatttcc tgctaacaga ttactctaat tcttctaggt 300
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aatacaatct atgataatgg ccaatagcaa acatttaatt agcactgttt cctgcctttg 420
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<213> Homo sapiens

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ctatattaat ataaaaataga aattgttaaa tatttcagga aaactttctg aaatataatt 180
tctccgtaca atgaaacagt ttttttcata tatctataaa tagatacagg agcctccagt 240
tatctaataga ggggttacata tgggtgcataa ttttaataacc atatttgttt catcttactt 300
caaatgtgaa agtacttttg ctataagttt cctaaaagta ttttaatactt ttttttttca 360
atttagatta aantcttgat gaacagtgtg tgggttgcaa aatttcaagg actggctgga 420
attttgagag agncatttca gcgtgatact ttggaancag tncctttaga cttgatgtta 480
aatgaantg taatgatggg cctgttccca tgctcatgtt tt 522

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gacttcctgt ttttgaaaag ccctggcagc caggaacaaa aatcaggagt gtggtagtgg 180
attagtgaag gtctcctcag gaaatctgaa gtctgtatat tgattgagac tatctaaact 240
catacctgta tgaattaagc tgtaaggcct gtagctctgg ttgtatactt ttgcttttca 300
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<400> 21
tccttttccc ggttccccgc

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<210> 22
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acacaacacg gtttcctttt

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<210> 23
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